

REPLACEMENT SHEET - A METHOD FOR OBTAINING
 CONSENSUS CLASSIFICATIONS AND IDENTIFICATIONS BY
 COMBINING DATA FROM DIFFERENT EXPERIMENTS

Vauterin et al.

Appl. No.: 10/758,249

Atty Docket: DECLE62.001A

Figure 3-A

	Experiment 1
Genotype 1	
Genotype 2	

$$\text{Similarity coefficient} = \frac{2}{3} = 66\%$$

	Experiment 1
Genotype 1	
Genotype 3	

$$\text{Similarity coefficient} = \frac{3}{4} = 75\%$$

	Experiment 1
Genotype 2	
Genotype 3	

$$\text{Similarity coefficient} = \frac{2}{4} = 50\%$$

Similarity matrix

	Gen 1	Gen 2	Gen 3
Gen 1	100		
Gen 2	66	100	
Gen 3	75	50	100

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Figure 3-B

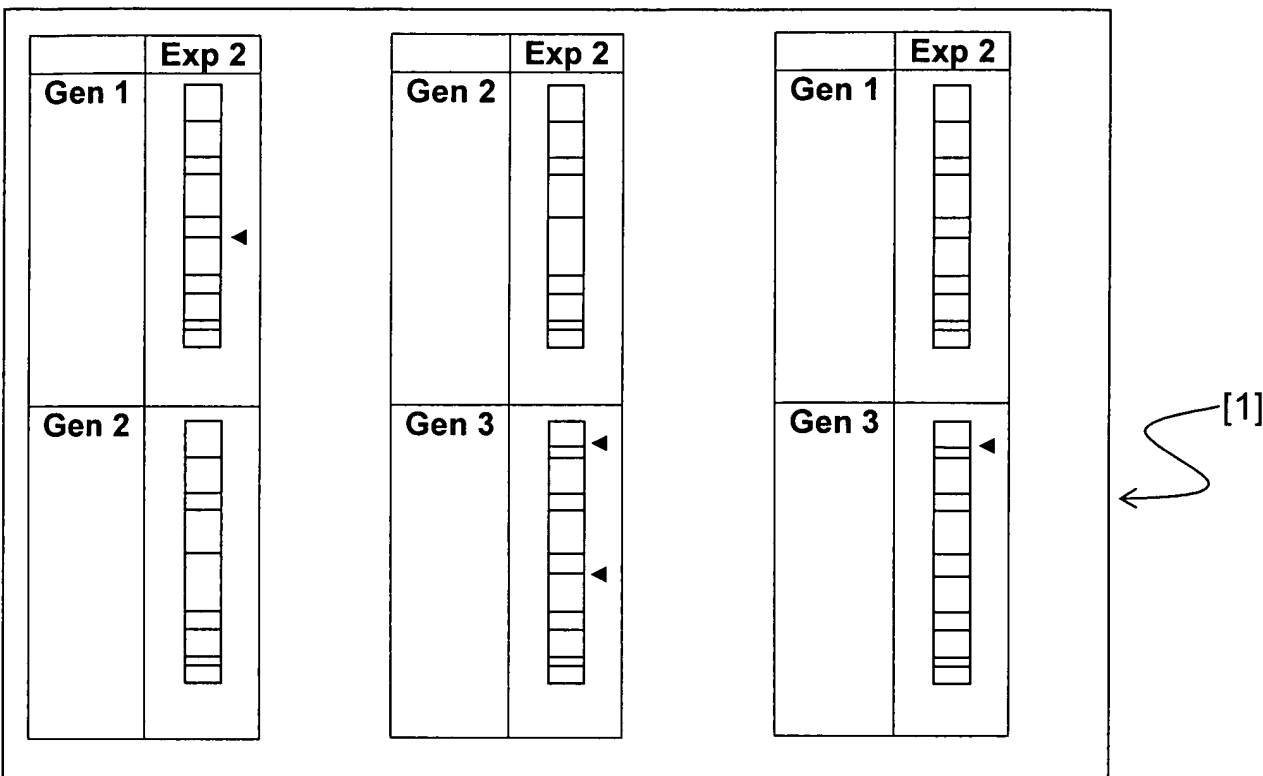


Figure 3-B displays two tables of experimental data, each showing two experiments (Exp 1 and Exp 2) for different generations (Gen 1, Gen 2, and Gen 3). The tables are arranged horizontally. Table 1 shows Gen 1 and Gen 2. Table 2 shows Gen 2 and Gen 3. A bracket [2] groups the two tables.

	Experiment 1		
	Gen 1	Gen 2	Gen 3
Gen 1	100		
Gen 2	66	100	
Gen 3	75	50	100

	Experiment 2		
	Gen 1	Gen 2	Gen 3
Gen 1	100		
Gen 2	88	100	
Gen 3	90	80	100

Figure 3-B displays a table of calculated consensus classifications and identifications for Gen 1, Gen 2, and Gen 3 across two experiments (Exp 1 and Exp 2). The table is arranged horizontally. A bracket [3] groups the table.

	Gen1	Gen2	Gen3
Gen1	100		
Gen2	$\frac{(3 \times 66) + (9 \times 88)}{3 + 9} = 83\%$	100	
Gen3	$\frac{(4 \times 75) + (10 \times 90)}{4 + 10} = 86\%$	$\frac{(4 \times 50) + (10 \times 80)}{4 + 10} = 71\%$	100

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FIGURE 4

